

FIG. 1.

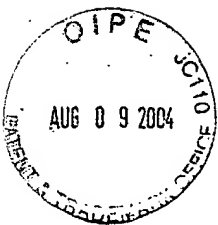


2/8

+

ABCG5	M	-----GDLSSLTPGGSMGLQVNRGSSQSSLEGAPAT-APEPHSLGILHASYSUSHRVR-PW-----	54
ABCG8	M	MAGKAAEERGLPKGATPQDTSGLQDRLFSSES DNSLYFTYSGQENTLEVRDLNYQVDLASQVPMFEQLAQ	70
ABCG5	---	WDITSCRQQWTRQILKDVSLYVESGQIMCIIIGSSGSCKTTLLDAMSGRLGRAGTFL-GEVYVNGRA	119
ABCG8	FKMPMTSPSC-Q	NSCELGIQNL SFKVRSGQMLAIIIGSSGCGRASLLDVITGR-GHGGKIKSCQIWINGQP	136
ABCG5	LRREQFDQFSYMLQSDTLISSLTVRETIHYTALLAIRRG-NPGSFQKKVEAMAEISISHVADRLLIGNY	188	
ABCG8	SSPOLVRKQVAHVRQHNQLLPNLTVRETLAFIAQMRLPRTFSQAQRDKRVEDVIAEIRLRQCADTRVGNM	208	
ABCG5	SLGCIISTGERRRVSI	AAQLIQD PKVMLFDEPTTGLDCMTANQIIVLLVEIARRNRIVVLTIIHQPRSEIFQ	258
ABDG8	YVRCLSGGERRRVSI	IGVQLIWNPEGILILIDEPTSGLDSTAHNLVKTL SRLAKGNRILVLSIHQPRSDIER	278
ABCG5	LFDKIAILSFCELTFCGTPAEMLDFFNDCCGYPCPEHSNPFDFYMDLTSVDTSKEREIEISKRVMIESA	328	
ABCG8	LFDLVLLMTSGTPIYIGAAQHMQVQYETAIGYPCERYSNPADFYVDLTSIDRRSREQELATREKAQSLAAL	348	
ABCG5	YDDSA-----	ICHKTIKNIERMKHLKT--IPM-----VPFKTKDSPGVESKLGVLIRRVTRNLVRNKLAV	386
ABCG8	FLEKVRDLDDFLWKAETKDLDEDTCESSVTPLDNTNCLPSPTK-MPGAVQQFTTLIRROISNDFRDLPTL	417	
ABCG5	ITRLLQNLIMGLFLLFFVLRVRSNVLKGAIQDRVGLLYQVFATPYTGMI	NAVNLFVPVIRAVSDQESQDQ	456
ABCG8	LIHGAECIMSMITIGE--LYFGHGSIQLSFMDTAALLFMIGALIEFNVIL	DVISKCYSERAMLYYELEDG	485
ABCG5	LYQKWQMMIAYAHVLPFSVVATMI	FSSVCYWTGLGHPHPEVARFGYFSAALLAPHLIGEFLLVLLGIVQN	526
ABCG8	LYTTGPYFFAKIILGELPEHCAYII	IJYGMPTYWLANIRPGLQPELLHFLLVWLVFCCRIMALAAAALLPT	555

FIG. 1C.



+

ABCG5 PNIIVSVVALLLSIAGVIVGSGFLRNIIQEM-PIPFKIIISYFTFQKYCSSEITVVNEFYGLNFTCGSSNNVSVT 595
ABCG8 FHMASFNSALYNSFYLAG-GEMINLSSLWTVB-AWISKVSELRWCHEGLMKIQFSRRTYKMPGLNLTIA 623

ABCG5 TNPMCAFTQGIQFIEKTCPGATSRFTMNFLILYSFIPALVILGIVVFKIRDHLISR-- 651
ABCG8 VS-----GDKILSAMELDSYPLIYAI-YLIVIGLSGGFMVLYYVSLRFIKQKPSQDW 673

Walker A Hotif
Walker B Hotif
Signature C-Hotif

ABCG5 Putative Transmembrane Domain
ABCG8 Putative Transmembrane Domain

FIG. 1C. (CONTINUED)



080904

4/8

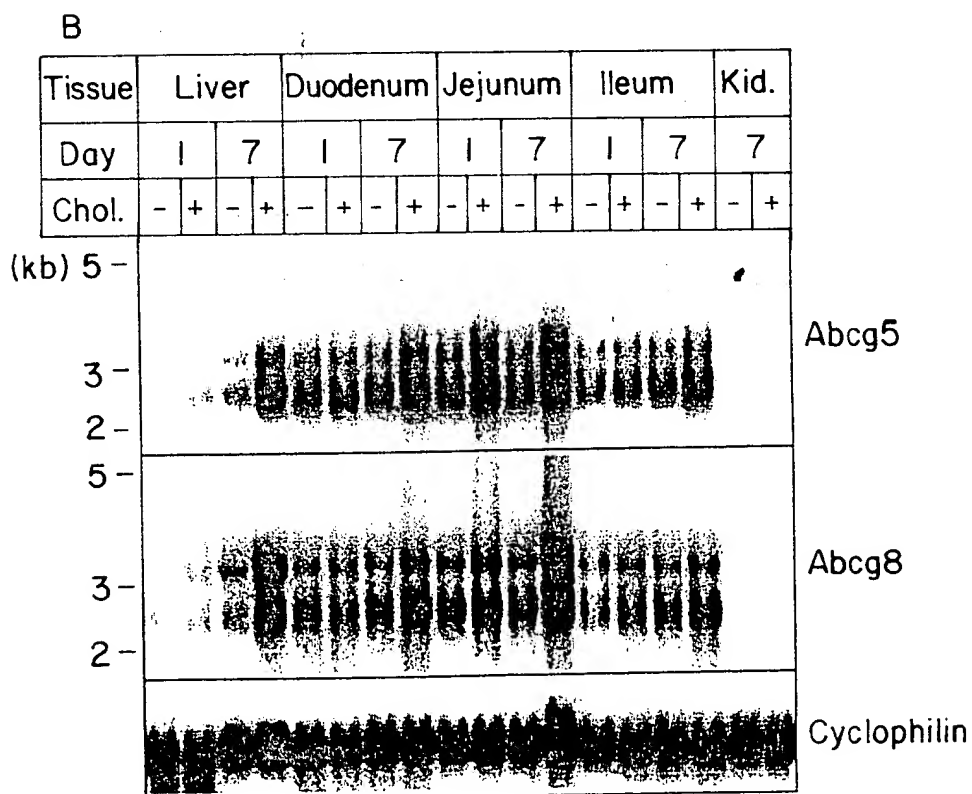
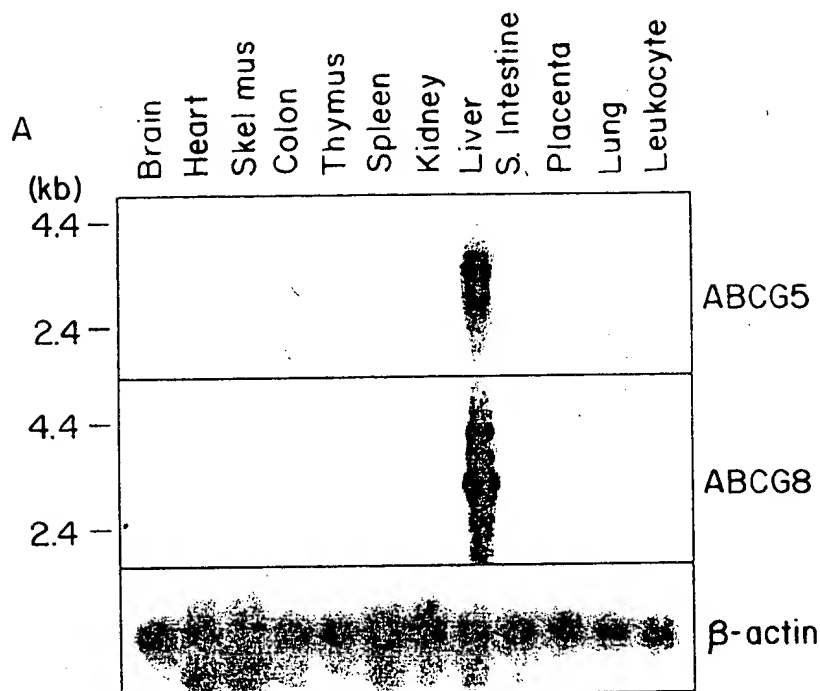


FIG. 2.

A ABCG8 exon 2 (reverse strand) thru ABCG5 exon 2 (forward strand)

[illegible]

FIG. 3.

+



6/8

gattttatatcctactcaggaaggagcatcaaaagacgtagaaggagtatttccccatagacgtctgcctcatggggattctga
cagcagagtgcctgtgctgtgtagtaggattgggtcaatctcaggcaatcctgtctccccatagaacaggggactgagggcgtcc
ctgttgaaatgtggccatcctgttctgtgtctccagaaaaagtgccgggtgtagaagctgggggaggggaggtcgtct
ttgctctgtcttccatactgccttctgcttcaaatcctgcccacaactcgagtcaaaaggccattatcaagcaaatgtttctcc
ggttaatgaggaaaggagcctagtagctccacttccctggccacctcgctctctgtccactctgcctccctccagaccataa
gactgcaagcacacaattctgacgctcccaaaacagcatcactatcacagccagtgatttgtaaaactgcctgaaaccaaagtgtg
tagccatagaaaatttcttctgtaataagagaaaaataaatcgtggctgggggaatggctcagttgtagaacacttggttca
acctccctgttacacacaggggggggagaaagtgggggagagaggaagaaagaaagagagagagagagagagagagagag
aggaaagtggccctcagagggatttatgacctgacttccagccgtgagccctgccctttcagtgaggtttctctaaagcagagcc
tcaactctacaaggtagcgagatgcctcaacccctccttgccattgttccctgacacctgccctttctctctctctctctct
ttgggtctgtctcctgcagcttctcagcctcacacagagacctttaggcttccccctggccttctcttctcctcctggttctca
ccaaaccaatgccaaggactaactactacataagtagtgcaagcgtagcgatcctgttggttaacctccccctgctctctgact
accactgagattcttggctgacagtcacatgggtcaacgctctgtgatggaatgtcatttggaaaaacatcaatccccggtcattc
acaggagcgtgctgtggaagtgacctcagaggtctcctggctcctgagactgttccccctcagaccatcaacactgagggag
acaggggccctgccccttccatttctacttgaagtcaggtggtacattaggaactaatcctgtgtaggaaagaaaaagtcag
tctgacactgcctccccctggcagagctcactcacCGAAGCATCTGAAGTACAGTCCCATTCACAGCTGGGTCTCTCTTTG
GTTTTCTCAGCCATgaccagtgctgttgtgcccttctgtggcctccccctgctgttggcctctctctgtcttctccttagag
ctggggcacctgagccctcctctgtgccagccttTCTCCCAGCATTCCTYTCGGCAACACTTCCTATAAACACACACCCGTGTGT
CTGCCATTGTTCGAGATAAGGACACTCTGGCTAAAGGTACATCAGATAATGGCATCGTTGGCCAAattggtgaactgttatctca
cgaggattccagggtggtaggatcgacagggcactccccattggctcctcagttaaagctgccctggagccggacagggccact
agaaaattcacttgcatctgttctctgtctagccATGGGTGAGCTGCCCTTCTGTAGTCCAGAGGAGCCAGAGGCCCTCACATCA
ACAGAGGGTCTCTGAGTCCCTGGAGCAAGGTTCCGGTACGGGCACAGAGGCTCGGCACAGCTTAGGTGTCTGCTGCTCCTA
CAGCGTCAGgtaaaggacctccacagcaaaaagctaggctctctgattgccttttctgaatgggtggggtggcctgtgggcttt
gggttctctgtccagcagatcagggtgaaagtggacagctctgtaacaaacagtgagtcgttctcctcctcctcctcctgcagggca
gagcctggacattaaaaacatgcctgcctgaagccgcttgccttctcactgatttctgctctcctcctcctcctgactcgccac
cacctgtcctgtgtagatggagaaggctcggagagtggggtgctgggggcaaaaaatggaatgaacactgctgaaggaaatgcag
gggtcacttcaagaagaaagcagtgtaggtgtaccatctcccagtcagagacccagtaatacagagcagcagtaatgggagggcatg
ctccttgggtgggtggccactgtcattatacctccaaggacacagagtggtacataaaggctaaaaacagagtggtcaacctgtc

FIG. 3. (CONTINUED)

+

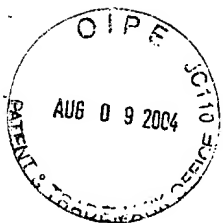
[illegible]

The 4 exons are underlined and the conserved regions are in uppercase. The sequence ends in intron 2 of ABCG5 and is in the following order:

ABC88	exon 2	(reverse strand)
ABC88	intron 1	(reverse strand)
ABC88	exon 1	(reverse strand)

FIG. 3. (CONTINUED)

+



Gap between genes

ABCG5 exon 1 (forward strand)
ABCG5 intron 1 (forward strand)
ABCG5 exon 2 (forward strand)
ABCG5 intron 2 (forward strand, partial)

B. Sequence Between ABCG5 and ABCG8 Containing the Control Sequences

Gaccagtgtgttgtgccccttgtgtggcctcccctgtgttggtggctctctgtctgtcttggctccttagagctggggcacctgag
ccctcctgtgtgccagccttTCTCCAGCATTCCTYCTGGCAACACACTTCCTATAAACACACACCGTGTGTCTGCGCTATTGTCTGA
GATAAGGACACTCTGGCTAAAGGTACATCAGATAATGGCATCGTTGGCCAAatttggtgaactgttatctcacgaggattccagg
ctgggtaggatcggacagggcactcccattggctcctcagttaaagctgcccctggagccggacagggccactagaaaaattcacttg
catttgcttcctgctagcc

FIG. 3. (CONTINUED)

+